Madras Agric. J. 91 (4-6) : 202-205 April-June 2004
https://doi.org/10.29321/MAJ.10.A00091

Relationship between expression of heterosis and parental divergen in rice

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Abstract: Fourteen *indica* rice genotypes studied for the genetic diversity were grouped into five clusters by Mahalanobis D^2 analysis. Cluster I consisted of ten genotypes, cluster II, III, IV and V consisteed of single genotype each *viz.* ADT 40, CR 1009, HA 891037 and Improved White Ponni respectively. Filled grains number per panicle followed by days to 50 per cent flowering contributed the maximum to the genetic divergence. Cluster III exhibited relatively high mean value for days to 50 per cent flowering and grain yield. The highest contribution to the maximum divergence was made by filled grains number per panicle followed by days to 50 per cent flowering and plant height. Hybrids between parents from inter clusters produced higher heterosis than the parents from intra cluster.

Key words : Indica rice, diversity analysis, expression of heterosis, correlation.

Introduction

Rice germplasm in India serves as a rich source of diversity due to the existence of high degree of phenotypic variability (De *et al.* 1988). It is generally accepted that the crosses between groups with maximum divergence would be useful for genetic improvement (Arunachalam, 1981). Hybrids showing strong heterosis were usually developed from parental lines, which are diverse in relatedness, ecotype, geographic origin *etc.* (Lin and Yuan, 1980; Yuan and Cheng, 1986 and Yuan, 1985). Genetic diversity can be evaluated with morphological characteristics, seed proteins, isozymes and DNA markers. Conventionally genetic diversity can be estimated by D^2 analysis, metroglyph and principal component analysis. Therefore, the nature and magnitude of genetic divergence and characters contributing to the genetic divergence were studied in fourteen *indica* rice varieties using D^2 statistics. Genetic distance between varieties correlated with expression of heterosis in their F_1 hybrids.

Materials and Methods

The materials used in the present study consisted of fourteen varieties (short, medium and long duration) of *indica* rice (*Oryza sativa* L.). All the fourteen parents were raised in a randomised block design with three replications in the field during *rabi* 1998 at Paddy Breeding Station, Tamil Nadu Agricultural Univer Coimbatore. Each parent was raised in i rows with 10 plants in each. Biometrical observati were recorded on important traits. The d were utilized for genetic diversity analysis usi D^2 statistics (Mahalanobis, 1936). Forty hybri were produced by crossing four lines (CR 100 ADT 40, CO 43 and Improved White Ponr with ten testers (ADT 43, ASD 20, HA 89103 IS 14, AS 95035, CB 97033, CB (DH) 9529 ACK 198, IET 15341 and TNAU 84143 Seeds from 40 cross combinations along wi fourteen parents were raised in randomised blo design with 3 replications during *kharif* ar rabi 1999. The mean values were used to estima heterosis per cent under three categories (Fonesc and Patterson, 1968). Significance of heteros was tested using the formula given by Snedec and Cochran (1967).

Results and Discussion

The mean values of seven morphologic characters (Table 1) of the fourteen paren were transformed into standardised uncorrelate values and D^2 values were computed for a pair wise combinations *i.e.* (14 x (14-1) 2=91 pairs). The genotypes were grouped int five clusters (Fig.1). Cluster I consisted ten genotypes *viz.* ACK 198, TNAU 84143 IET 15341, AS 95035, IS 14, ASD 20, C 97033, CO 43, CB (DH) 95298 and AD 43. Four genotypes *viz.* ADT 40, CR 100

Table 1. Mean values of the quantitative traits of parents

Parents	Days to 50% flowering	Plant height (cm)	Number of productive tillers/plant	Panicle length (cm)	Number of filled grains per panicle	Hundred grain weight (g)	Grain yield/ plant (g)
CR 1009	130.74	98.69	13.83	23.13	128.52	2.17	31.03
ADT 40	100.60	117.16	13.08	22.46	101.29	2.71	21.00
CO 43	114.43	80.70	16.47	18.40	140.36	2.03	30.79
I.W.Ponni	111.60	117.46	14.56	23.60	209.76	1.53	25.03
ADT 43	74.33	76.96	15.46	22.06	142.78	1.86	26.71
ASD 20	84.33	79.26	13.50	21.65	100.13	2.14	25.28
HA 891037	70.00	71.26	10.46	19.31	70.85	2.02	16.73
IS 14	94.16	73.33	13.69	21.36	107.46	2.45	19.90
AS 95035	99.66	77.32	16.45	20.36	120.33	1.92	20.23
CB 97033	98.16	81.70	14.05	23.25	150.16	1.89	24.49
CB (DH) 95298	102.16	88.86	14.66	21.46	122.50	2.50	16.63
ACK 198	99.50	93.93	14.06	21.26	102.13	2.20	28.56
IET 15341	101.33	80.78	17.27	23.95	100.56	2.18	27.69
TNAU 841434	98.16	90.14	12.85	22.18	115.73	2.68	29.42

Table 2. Estimates of average intra and inter cluster D^2 for the cluster constructed from fourteen genotypes

Clusters	I	II	III	IV	V
I	56.28	82.84	87.15	101.13	168.10
II	82.84	0.00	77.04	128.99	161.49
III	87.15	77.04	0.00	161.69	140.83
IV	101.13	128.99	161.69	0.00	249.17
V	168.10	161.49	140.83	249.17	0.00

Table 3. Mean values and contribution of biometrical traits to the total divergence

Characters	Clusters					Contribution (%)
	I	II	III	IV	V	
1. Days to 50% flowering	96.63	100.60	130.74	70.00	111.60	20.88
2. Plant height (cm)	82.30	117.17	98.69	71.27	117.47	17.58
3. Productive tillers number per plant	14.85	13.09	13.83	10.47	14.57	1.10
4. Panicle length (cm)	21.59	22.47	23.13	19.32	23.60	0.00
5. Filled grains number per panicle	120.24	101.29	128.52	70.85	209.77	51.65
6. 100 grain weight (g)	2.19	2.71	2.18	2.03	1.54	1.10
7. Grain yield plant (g)	24.97	21.00	31.03	16.73	25.03	7.69

HA 891037 and improved white ponni remained individually in four clusters. The average intra and inter cluster D^2 values are presented in Table 2. At the intra cluster level, the maximum D^2 value (56.28) was noticed in cluster I. Whereas in clusters, II, III, IV and V the intra cluster distance was zero, because all these clusters had only one genotype. At the inter cluster level, the maximum D^2 distance (249.17) was observed between clusters IV and V followed by clusters I and V (168.10). The least inter cluster distance (77.04) was recorded between cluster II and III. Classification of rice varieties based on duration groups was reported by Vairavan et al. (1973). The four genotypes which deviated from cluster I had distinct characters. The genotype

Table 4. Superior hybrids based on average (di), better (dii) and standard (diii) heterosis for grain yi

Hybrids	*Per se* performance	Heterosis		
		di	dii	diii
CR 1009/ADT 43	41.87	58.04**	50.51**	49.17**
CR 1009/HA 891037	57.98	177.10**	108.45**	106.59**
CR 1009/CB (DH) 95298	38.87	65.80**	39.72**	38.48**
CR 1009/IET 15341	40.13	41.15**	38.15**	42.99**
CR 1009/TNAU 841434	50.77	94.51**	82.50**	80.88**
ADT 40/ADT 43	43.25	63.93**	56.70**	54.10**
ADT 40/AS 95035	45.43	89.97**	64.61**	61.88**
ADT 40/CB (DH) 95298	38.98	67.07**	41.24**	38.90**
ADT 40/TNAU 841434	41.20	58.51**	49.28**	46.79**
I.W.Ponni/IET 15341	46.97	66.84**	61.68**	67.34**

** Significant at 1% level

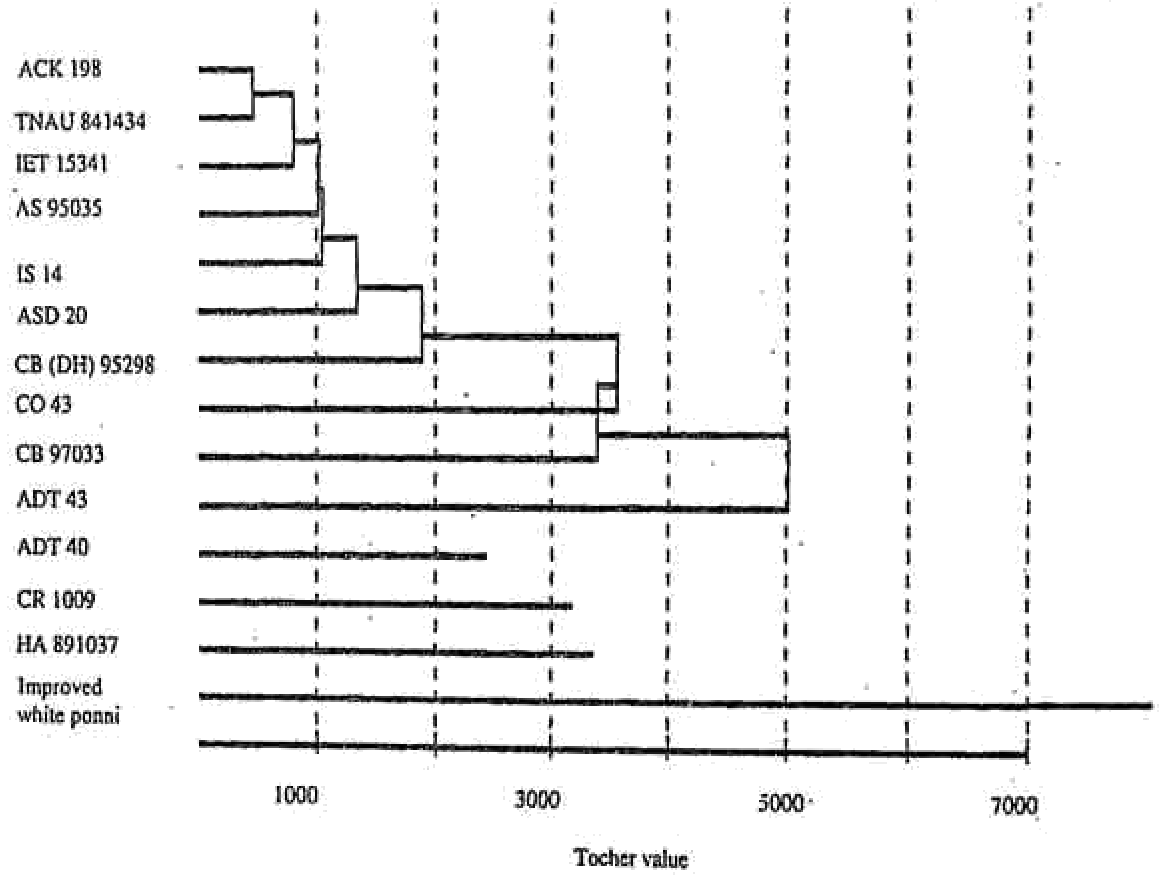

Fig.1. Genetic diversity analysis of fourteen genotypes

CR 1009 formed a separate cluster due to its long duration and more filled grains number per panicle (128.52) and ADT 40 recorded medium duration with moderate filled grains per panicle. Likewise, the genotype HA 891037 recorded very low filled grains (70.85) and also had very early duration in flowering and formed a separate cluster. Similar results were reported by Sardana *et al.* (1997). Highest filled grains number per panicle (209.77) was recorded by improved white ponni, which also remained single in a cluster. The divergence of these four genotypes from the genotypes in cluster I may also be due to the involvement of different ancestral pedigrees or uncommon parentage. In cluster I, all the 10 genotypes except two (IS 84 and TNAU 841434) have IRRI cultivars in their parental ancestry. The four genotypes *viz.* ACK 198, TNAU 841434, IET 15341 and AS 95035 in cluster I also had a common parent Peta in their ancestry which may be a reason for close relationship among them. Cultivars grouped together in a same cluster were related by pedigree was also reported by De *et al.* (1988).

The mean values of different characters the different clusters are presented in Table Cluster III had the highest mean value for days to 50 per cent flowering and grain yield, whereas Cluster V had the highest mean value for plant height, panicle length and filled grains number per panicle. The values for productive tillers number was higher in cluster I. Cluster I had the highest mean value for 100 grain weight.

The amount of contribution made by the seevn traits towards divergence was calculated. The highest contribution was made by filled grains number per panicle (51.65 per cent) followed by days to 50 per cent flowering (20.88 per cent) and plant height (17.58 per cent) (Table 3). Ramesh and Bateshwar Kumar (1998) reported that grain yield per plant, total spikelets, seeds per panicle and grain weight per panicle were mainly responsible for genetic divergence.

The 40 F_1 hybrids produced from the above parents revealed that though all combinations of parents had heterotic effects, particularly the hybrids of parents from different cluster produced high heterotic value (Table 4) in the cross combinations *viz.* CR 1009/HA 891037 and CR 1009/TNAU 841434, etc., as they had high significant effect on all the three categories of heterosis for grain yield. Lin and Yuan (1980) reported that the level of genetic diversity between two parents has been proposed as a possible predictor of F1 performance and heterosis in rice. The results obtained from morphological characters for studying genetic divergence have not been consistent in demonstrating the relationships between the divergence of parental lines and magnitude of heterosis (Li and Ang, 1988 and Virmani *et al.* 1994) because, they are influenced by type of material, selection of traits *etc.* Often the traits that contribute more to divergence have the little to do with a complex trait such as yield. To circumvent this problem an alternate approach of diversity analysis using isosyme or molecular markers can be practiced. However, the present study revealed that parents from diverse pedigree or parents with more genetic distance produce good heterotic hybrids. Thus, while selecting the parents more importance is to be given to the diversity of the parents to get enhanced heterosis.

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(Received: December 2002; Revised: June 2003)